

SEARCH REQUEST FORM

Requestor's Name: Ruixiang Li Serial Number: 684725
Date: 9-12-01 Phone: _____ Art Unit: 1646
3D05

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

*Compare Seq ID 1 with
version 1 of ACCOBS 71*

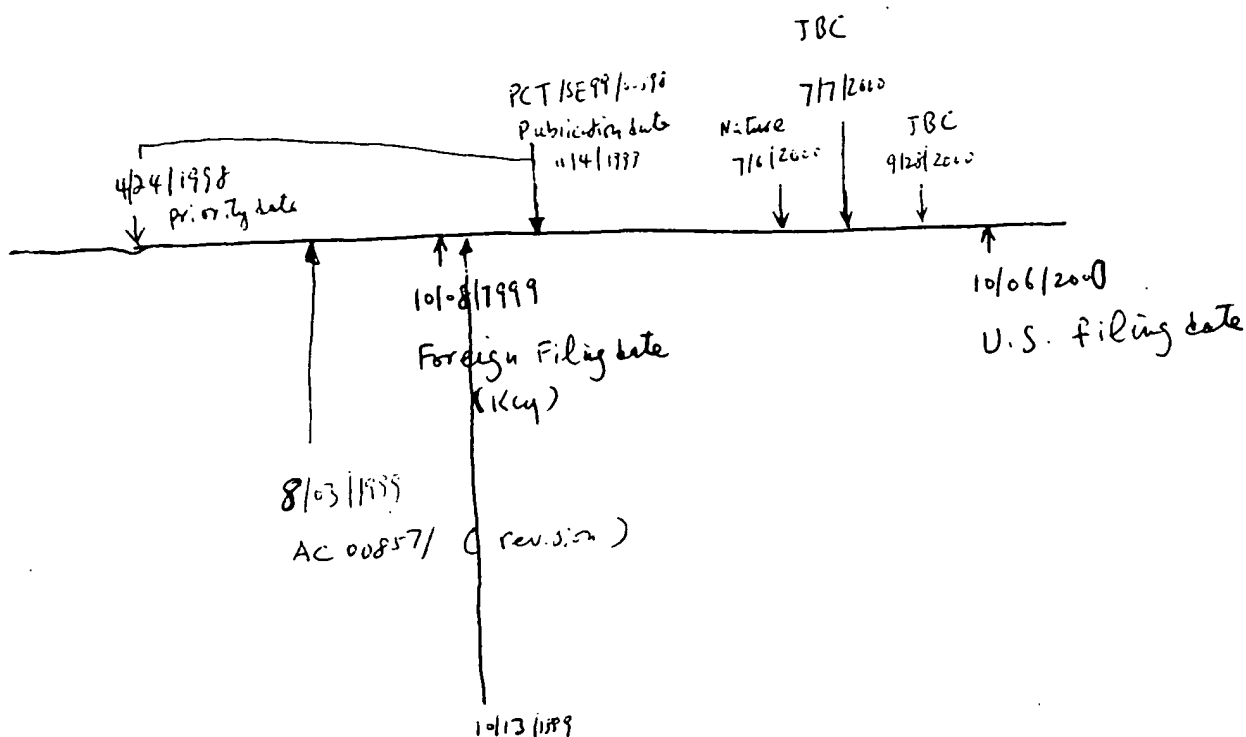
POINT OF CONTACT:
BARB O'BRYEN
TECH. INFORMATION SPECIALIST
STIC CM1 12C14 308-4291

STAFF USE ONLY

Date completed: 9-12-01
Searcher: PCB
Terminal time: 130
Elapsed time: prep 40
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ ☒ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ GCG Other Internet



AC 008571
 Version AC 008571.1
 GI: 5686496

- Submitted (03-Aug-1999)
- ① Public Domain Date:
 before 10/13/1999 ?
 - ② Align with SEQ ID 1

Ex Li,

The program I used to
 compare Seq 1 of 09-684725 to
 AC 008571, version 1 can only
 handle 32,000 nt long sequences.

Version 1 is 318,807 nt long,
 so I had to break it into 7 parts
 & compare each of the parts to Seq 1.

Bases 204888-205616 match
 the complement of Seq 1.

Barb



Nucleotide

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search <input type="text" value="Nucleotide"/> for <input type="text"/>		<input type="button" value="Go"/>		<input type="button" value="Clear"/>			
<input type="button" value="Limits"/>		<input type="button" value="Preview/Index"/>		<input type="button" value="History"/>		<input type="button" value="Clipboard"/>	
<input type="button" value="Details"/>							
<input type="button" value="Display"/>	<input type="text" value="GenBank"/>	<input type="button" value="as"/>	<input type="text" value="HTML"/>	<input type="button" value="Save"/>	<input type="button" value="Add to Clipboard"/>		

□ 1: AC008571[gi:5686496]

```

LOCUS       AC008571       218807 bp       DNA       HTG       26-JAN-2000
DEFINITION  Homo sapiens chromosome 5 clone CTC-550M4, LOW-PASS SEQUENCE
             SAMPLING.
ACCESSION   AC008571
VERSION     AC008571.1   GI:5686496
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      human.
  ORGANISM  Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 218807)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Human Chromosome 5
  JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 218807)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL    Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
             Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     [WARNING] On Mar 9, 2000 this sequence was replaced by a newer
             version gi:7211884.
             -----Genome Center
             Center: Joint Genome Institute
             Center Code: JGI
             Web site: http://www.jgi.doe.gov

```

* NOTE: This record contains 42 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

```

*      1      760: contig of 760 bp in length
*                gap of unknown length
*      761     1587: contig of 827 bp in length
*                gap of unknown length
*     1588     2375: contig of 788 bp in length
*                gap of unknown length
*     2376     3130: contig of 755 bp in length
*                gap of unknown length
*     3131     3929: contig of 799 bp in length
*                gap of unknown length
*     3930     4664: contig of 735 bp in length
*                gap of unknown length
*     4665     5908: contig of 1244 bp in length
*                gap of unknown length

```

or
ws
t

Ex. Li -

This sequence
record was 59 pages
long, so I didn't print
all of them, but wanted
to show you that I was
able to retrieve the
correct record.

Bank

```
*      5909      6642: contig of 734 bp in length
*                  gap of unknown length
*      6643      7928: contig of 1286 bp in length
*                  gap of unknown length
*      7929      9764: contig of 1836 bp in length
*                  gap of unknown length
*      9765     11784: contig of 2020 bp in length
*                  gap of unknown length
*     11785     13491: contig of 1707 bp in length
*                  gap of unknown length
*     13492     15107: contig of 1616 bp in length
*                  gap of unknown length
*     15108     17115: contig of 2008 bp in length
*                  gap of unknown length
*     17116     18946: contig of 1831 bp in length
*                  gap of unknown length
*     18947     20113: contig of 1167 bp in length
*                  gap of unknown length
*     20114     21818: contig of 1705 bp in length
*                  gap of unknown length
*     21819     23699: contig of 1881 bp in length
*                  gap of unknown length
*     23700     26482: contig of 2783 bp in length
*                  gap of unknown length
*     26483     29112: contig of 2630 bp in length
*                  gap of unknown length
*     29113     32185: contig of 3073 bp in length
*                  gap of unknown length
*     32186     35668: contig of 3483 bp in length
*                  gap of unknown length
*     35669     38521: contig of 2853 bp in length
*                  gap of unknown length
*     38522     41445: contig of 2924 bp in length
*                  gap of unknown length
*     41446     44435: contig of 2990 bp in length
*                  gap of unknown length
*     44436     49095: contig of 4660 bp in length
*                  gap of unknown length
*     49096     52340: contig of 3245 bp in length
*                  gap of unknown length
*     52341     58964: contig of 6624 bp in length
*                  gap of unknown length
*     58965     67289: contig of 8325 bp in length
*                  gap of unknown length
*     67290     76424: contig of 9135 bp in length
*                  gap of unknown length
*     76425     82934: contig of 6510 bp in length
*                  gap of unknown length
*     82935     92710: contig of 9776 bp in length
*                  gap of unknown length
*     92711     99976: contig of 7266 bp in length
*                  gap of unknown length
*     99977    111110: contig of 11134 bp in length
*                  gap of unknown length
*    111111    119820: contig of 8710 bp in length
*                  gap of unknown length
*    119821    131057: contig of 11237 bp in length
*                  gap of unknown length
*    131058    140629: contig of 9572 bp in length
*                  gap of unknown length
*    140630    155583: contig of 14954 bp in length
*                  gap of unknown length
*    155584    167555: contig of 11972 bp in length
*                  gap of unknown length
*    167556    184185: contig of 16630 bp in length
```

```

*          gap of unknown length
* 184186   201363: contig of 17178 bp in length
*          gap of unknown length
* 201364   218807: contig of 17444 bp in length.

FEATURES             Location/Qualifiers
     source            1..218807
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="5"
                        /clone="CTC-550M4"

BASE COUNT    66620 a  42793 c  41952 g  67204 t    238 others
ORIGIN
1 gatataatat cgatcccctc actggctcta aagaacaaat acagcaacgt ggatttcaat
61 taagattctg ccatcccatc gatagagttc tcttaatcct tctttagagg tgctgcctgg
121 gtaataaaac cttcatgctg caggctgtag gcaggtttgt ttaacccgag cttaaactgac
181 aaagctctct gagacatgct cacctgctta gaatctgtgc atcacctcct attggctgtg
241 tgtggggcat tgcgatgcct ccatgtggta caggaggctg gcctaagagt tctgaactgc
301 aaaccttcac aggaaattct tgggctggct ggccacctgg cttacgttat ttattttatt
361 atttagttag ttgtttttat tgcttttagg gtctgcacct gatggtggca gtgaggagg
421 ttgaggtgag cttccatctc ttggaatccc accattccta ttcaactcat gtcaaattaa
481 attaatacta tttccatgtg aataattgaa gatatttcct caactttaaa aatgtgaaa
541 aaggcatctt ttagaaaata tttgctgttt aaaaaatact agccatgcac aatccagata
601 agaagaatgt agtttgagac gagttcctgt gaagattatc accctaagcc actcctgtat
661 atatgtttcc ctactgacac ctgctcatcc ttctttgctt cattctatgg
721 ctaactccta agcacaggga tgcaattctg tctggagatc gaagagaaaa ggaggggngg
781 ggnnnntttt agaaccctn  gatgtgacgc atcgctaagt gctctaaatg taccagcct
841 tacaacata  ttctatcact ccatgtctg  tgaccatagc agaaattagc aatcaatcat
901 agaagttgtt cctcctgggc ctggatgtgg cttcacaaag tctcacagcc actgtaccag
961 tgggtcagac tctaaaccga ggaatacaca tgtacacacg cagatacatg ggtgtgtgtg
1021 tttgtgtgtg tgtgtgtttg ttttaatat  ataaggccct atattcctga tggtgacttt
1081 gaaaaaaatc acttgtgctc tgtggtccta agtttttttt tttttttatc tgaaagagga
1141 aatttgagtt ctttagtcta ctagtggaa  aagcacaaag ggctgtcac  tgcagtgtg
1201 ttttctgggg ctcaagttaa caagagacaa atcacagatt caatcaaaag ctgcatgtgg
1261 aaggctcaat accatttttt gagaaaagga aaccttgggg ttattcatct tcacctcata
1321 ggaatcaagc agaaatagaa attacctttc aggagaagga atatataact tacagctttt
1381 tgagatcggc tttacattta ttttttctta ttcaatctag ttcctttatg gaacataaat
1441 taaccttaaa gagtagcact ggagaagagg gaaagaatat tgcgatttct ctctctctac
1501 aatttaaagt ttaaaaatca tagttatctt ttctttattt atcaaaaggc tatgacctct
1561 cagagcaatt gtgtaagcaa cccaaaaggg ggnatagggg nttcgtagac gtactcctat
1621 agtgctctaa agcttgggat gaggtatttt gcatatgtgt tcttagatac gttgaacaac
1681 aagaatgccca agataatcct gaatcctttg ggattacaca agtggcccat tttcccttac
1741 ttgatggctg tgaagaaacc ctaagtgcag taggtccctt aaaatgcaat gctggctttt
1801 ctgaggatct atcctaacct cttttctagg caccagatca ataactcatg taacatctca
1861 tcatgaccca actggaaaag ttacggatat gctaaaagag aagatggagt ctgagccagt
1921 ggaaccataa atgtgggtta caggttctgg aacctagaga atcttttgtt tagataaagg
1981 tggagaggaa tggattataa agttaggtaa gaggatttgt tggatatggg cagtattctc
2041 aggcaagatt taacacactg aaaagactct gggagaaggt tctaataatt tgccacaagg
2101 tgggggaaaa atttaaaaaa tttttttttt tttttttgaa actggaaaaa acataccaac
2161 cttaaaaatg aaatagcaaa attgccttgc caactgggga gaatagatca acaggcacgg
2221 agaaatgggt atactagaat gtttctactt catatttaaa aaactactgg ctgattaaat
2281 tcctcaaaag ggctcagagg acgttcattt tactaaagaa ttaaaaaatg cagtacctac
2341 aacactgctc caaagaaagc aacgggccag gttttccagc gacttgttgc cgatccctaa
2401 nactctaaat agcagnnngn ncaaccacac cttaaactgac aaagctctct gaaacatgct
2461 cacctgctta gaatctgtgc atcacctcct atnggctgng tgtggggcat tgcgatgcct
2521 ccatgtggta caggaggctg gcctaagagt tctgaactgc aaaccttcac aggaaattct
2581 tgggctggct ggccacctgg cttaggttat ttattttatt atttagttag ttgtttttat
2641 tggcttttag gtctgcacct gatggtggca gtgaggagg  ttgagtgag  tttccatctc
2701 ttggaatccc accattccta ttcaactcat gtcaaattaa attaatacta tttccatgtg
2761 aataattgaa gatatttcct caactttaaa aatgtgaaa  aaggcatctt ttagaaaata
2821 tttgttgttt aaaaaatact agccatgcac aatccagatt agaagaatgt agtttggag
2881 gagaaaaccc ccccgaaaaa aataaaaaag aaatttcctg gaagatatca cctaagcact
2941 ctttatatag tttccctact gacacctgct catccttctt tgctcattga cagcatctag
3001 tggtagctct agccagngat ccattctgcc tgagatcaga tatcctccaa gagcacaac
3061 aggtagaaat ggcattcata taggggctgt acagtgtgtt gctgagagat gtatataaat
3121 ttcttgagat acgaaagtc  tccgccgtca tctaacatct caaanacan  aannatggct

```


GAP of: us-09-684-725-1 check: 1088 from: 1 to: 729
FROMIG of: /home/bobryen/Dig/US09684725.seq
sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 64001 to: 96000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.cmp
Compcheck: 8760

Gap weight:	50	Average Match:	10.000
Length weight:	3	Average Mismatch:	0.000
Quality:	2460	Length:	32000
Ratio:	3.374	Gaps:	4
Percent Similarity:	36.900	Percent Identity:	36.900

Match display thresholds for the alignment(s):

1 = IDENTITY
- = 1

us-09-684-725-1 x version1 September 12, 2001 10:34 ..

```
1 .....atgaaaaac 10
89801 ataaattcttcttctgttgaattgtacatcattgtggtgtgtg 89850
11 ttccagaatgtcttctgtatccagcagaaactagaatcattccag 60
89851 ctgagaacaatgagacactgttccaatgacatataagagctcagggc 89900
61 aaacacctgaaacagacgagagatctgacctctctctcgagacctcg 110
89901 tggaaaagaatttgagagtgtaagccttaagtctgtctgtgagcgca 89950
111 gcgcagcacacttctctcccggtctgtgtgtatgtgccaatcttg 160
89951 tccctttttaacaacatgaacttttctcaatttgcctctgtgtca 90000
161 tggcgggggcatctgcaatgtcctgtgtgctgagatctgcagcac 210
90001 cgctccctgaacgtgaatcaatcaatcattttagtgatctcttgaca 90050
211 caggctatgaagacgcccacaactactactcttcagcctgcgctc 260
90051 gtgtcagctctgcttaagctccctttttaacttaagcttgact 90100
261 tgaactcctgtctgtctcttgaaatgcccctggaaggtcataagatgt 310
90101 ttctcttctgtctctctgtgtatgcaaaaaaacaagcgtgtgtt 90150
311 ggcgcaactaccct...tctgttcggggccggtgggctgtactaacg 357
90151 ttctatactaatgtttatatatttttggagcgagatgaacaatcaca 90200
358 acggccctcttgagacggtgtgtctgcctccacactcagcatcaccac 407
90201 tactctgcttctgtctgtgctgcatcttacttaaatctgacttatt 90250
408 cgtcagcgttgagcgtacgtgagcatctacacccgttcggcgccaaac 457
90251 tatcagaatttaactcagacacttctctcagaacctgcacatgacc 90300
```

```
458 tgcagagacccc-ggcggcgccctcagagatcctcggcatcgtctggg 506
90301 cagacaacacccctgtttatgatccacagcacccctgaattcctttg 90350
507 ctctcgtgtcttctctccctgcccacacacagacatcattgcatcaagt 556
90351 cagcccttgttcaaccagcaattatacagagataattatgtttctcaca 90400
557 tccaacttccccaatggtc....cttgtccaggttcggccaact 601
90401 agtatatacttctagaggcgaggaacttctgtctagtccacacatgt 90450
602 gtac-ggtcactcaagcccagtgatctacaaattcattcaccaggtcac 650
90451 atactagtcactgtgcttaatgacatttatacaaatctcatgagagcat 90500
651 ctcttctatcttaccctccccaatgactgcatcagtgctctact 700
90501 ctctgtgtatcagccatgtagtactgtgaaacagatagattagctcctc 90550
701 acctcatgcaactcagagtgatctag..... 729
90551 agctcgtgaaactatagctcagtgaggttttcaattcttcttctccccc 90600
```


GAP of: us-09-684-725-1 check: 1088 from: 1 to: 729

FROM: of: /home/bobryen/Big/US09684725.seq
sequence 1, application us/09684725

general information:

applicant: lee harland

title of invention: novel polypeptide

file reference: pcs10361adam

to: version1 check: 7472 from: 96001 to: 128000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/wsgapdna.comp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2441 Length: 32001

Ratio: 3.348 Gaps: 6

Percent Similarity: 38.187 Percent Identity: 38.187

Match display thresholds for the alignment(s):

IDENTITY
5
1

us-09-684-725-1 x version1 September 12, 2001 10:28

```

1 ..... atgaaacttcagaatgtctctgcat 29
105351 tgcacgtgagctctctgctgcatgtatcttcttctgctctctgccc 105400
30 ctaccagcagaactaagaatccatccagaacactggaacagcagc 79
105401 tgaacaaaca.caagtcaactgtctccagatctctataactctatacaact 105449
80 aggaagatctggc..ctcctctcggaacctcgcgccagcagcactctctcc 127
105450 actactcttctccctgaacctcaacagcaaatcattgtagtcacttcagct 105499
128 tccccggtcgtggtgtaigtgccaattttgtgtgggggtcattgac 177
05500 tgcgtgctatcctctccacagatattctacctgctgtagtaaat 105549
178 aatgtcctggtgctgtggtatctgacagcagcaggtatgaagagcgc 227
105550 tcaagcagcgttcaacattctgttctatccagtagtcaataatccatc 105599
228 caccactactacactctcagcctggtcggtctctgacctctgtctctgc 277
105600 cagtcactctcagaagcttgacatcaactaaccactaccagactgtgca 105649
278 tccctggaatgcccttgaggtctatagatgtgtagcgaactacccttc 327
105650 gaagggagaagagcttccatgtctcctgtagtctctatcttggaatccatc 105699
328 ttgttcggcccggtggcgtgtaacttcaagaagcgcctcttgagaccgt 377
105700 tctaaagaagaagcttggaatgttatttttgatagtcctcctccgtaataag 105749
378 gtgcttgccctccatctcagatcaccacacgcgttgagcgctagc 427
105750 ccagtgctataaagaacaattcagaagtagtactgtgctaaattgaatt 105799
428 tggcactctaacccggttcggcgcaactgagagaccccgcgccgg 477
105800 tatcaaaccttgaacttctcatttcatgtagcactctctcctaataagac 105849

```

```

478 gccctcaagatcctcgcatcgtctgggcttctcgtctcttccct 527
105850 aatctctacttcatctggtgcatccctgtgtatatacacaactagacct 105899
528 gcc..caacaccagcatccatggacatcaagtccactact....cccc 570
105900 tcccttagtataactacttacttccaaatcaactatttatatactc 105949
571 aatggtccctggtcccaaggttcggcaact..gtacggatcaagacc 618
105950 attgagatcataatcttctatcttctgtagtgccttccaattatctc 105999
619 atgtgacttacaatttcaatccaggtcaacctctctctatctact 668
106000 attgtaactactctgtttgttaactcttcaattctcccttctctatatt 106049
669 cctcccaatgactgtcatalcagtgctcttactacc..taatggacatcaga 717
106050 ccttcttaactctccatgatatatttaaaacaccttaatggaactcca 106099
718 gtgagatctag..... 729
106100 ttgttctctattctattcttgaatttttctcaatgaccttcaagc 106149

```

GAP of: us-09-684-725-1 check: 1088 from: 1 to: 729

FROMIG of: /home/bobryen/Big/US09684725.seq
sequence 1, application us/09684725

general information:

applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 128001 to: 160000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/twsgapdna.comp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2461 Length: 32002
Ratio: 3.376 Gaps: 9

Percent Similarity: 42.641 Percent Identity: 42.641

Match display thresholds for the alignment(s):

1 - IDENTITY
5
1

us-09-684-725-1 x version1 September 12, 2001 10:36

```

1 .....atgaaaaacttcagaatgtcttcctgatacta 32
156901 aagagggaataactataataatgaataatgaatgattcctaagaatg 156950
33 ccagcagaactagaagaatccatccagaacaacatg..... 69
156951 tggagacgtgattgattgaatgagtgagaagaagtgctcctgaggttct 157000
70 .....aacagcaccgagagatctgacctctctcgcgacc 107
157001 gaccagtgctcctaagtacggtgggaccttcaacttaagaagaacat 157050
108 tcgsgcgcgcacatctctcccccgtctgtgtgtatgtgccaattt 157
57051 tagaggtggaagaagttcagaagaagaacaagattcccttgcacat 157100
158 ttgtgtgggggtcattggaatg...tcctgtgtgctgtgattctgc 205
157101 aagaggttcacatgtgtgggtgactgaactgactgaactatgcatacaga 157150
206 agcaccaagctatgaagaagcccaactactactcttcagcctggcg 255
157151 ttcccca.tcaggaatgagctccctccactattcgtctttagacaggg 157199
256 gtctctgacctcctgtctctctctctgaaatgcccctggaagtctatga 305
157200 gtccccaaccccccgccacagaccagatcacatcagcctgttagga 157249
306 gatgtggcgcaactaccccttctctgttcggcccggtggcgtgacttca 355
157250 actgtgtcacaagggaaggtgagtgacgggcaagcaagtgcttactgctga 157299
356 .....agaagccctctttagaacctgtgtctgcgc.tc 389
157300 gctcatgcaaggatcagtgctcctttagaatacctaactaacgcctta 157349
390 catctcagcatcaaccgctcagcggtgagcgctacgttgccatccctac 439
157350 tgatctgaggtggaacagtttatctctgaacaacatcctcccaacttctc 157399
440 accggtccgcgcacaacttgagagacaccggtgcgcccgtcccaagatc 489
157400 cctctctcccgacagaacagtggaataaaactgtcttccacaataaccatc 157449
490 ctcgg.....catcgtctgggtctctccgtgtctcttctcccgcccaa 533
157450 ctgggtgccaaaaacgltgggggtgctggaagaatgtctcagctgaa 157499
534 .....caccagatcatgcatcaatgtccactacttcccca 572
157500 gaagtgtgtcctcaactgtccatccagtgactcgagagataaagatcccca 157549
573 tgggtccctgtgtcccaaggttcggccacctgacgtlcatcaagcccatgt 622
157550 ttcagccaactcagagcagctctgaggggtcagttcagc.tgcacagtt 157598
623 ggaatcaaatcattcatcagatcaccctctctat.tctactcct 671
157599 cctggggcgtctgcatctcccttggcccaactacttgttcttctct 157648
672 cccatgactgtcatcagtgctcctctactactcaatggcactcagagtga 721
157649 ttccagatgtggaatccctgagagcttcatgtcctaataaacctgactgc 157698
722 gtaactag..... 729
157699 taattcccccaagagtgctgtgcttgagcaacaacaacgtgtgacacag 157748

```


GAP of: us-09-684-725-1/ check: 1088 from: 1 to: 729

FROM: /home/bobyen/big/US09684725.seq
Sequence 1, application us/09684725

General information:

Applicant: Lee Harland

Title of invention: novel polypeptide

File reference: pcs10361adam . . .

to: version1, check: 7472 from: 192001 to: 218807,

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.cmp
Compcheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2610 Length: 26807
Ratio: 3.580 Gaps: 0

Percent Similarity: 35.802 Percent Identity: 35.802

Match display thresholds for the alignment(s):

1 - IDENTITY
5
1

us-09-684-725-1 x version1 September 12, 2001 10:39 ..

```
1 .....atgaaaacttcagaatgcttcttgatcta 32
204901 ctgagtcgcatgagtagtagagagacactgtagacatgcatgaggagag 204950
33 ccagcagaaaactagaaagatccatccagaacactgnaacagcacccagag 82
204951 gtagaataaggaagaggtgaccctgagatgaaatgtagatccaatg 205000
83 agtatctgacctctctctgacgacctcgccagcgaacttctctctccc 132
205001 gcttgatgaccgtagacaggtggcgcgaacctgagcagaggaacccattg 205050
133 gtgctggtggtgtagtgcgaatttctggtggtggtggtcattggaatgt 182
205051 aagtagtgaacttgatgacatgagatgctggtggtggtggtgaggaagag 205100
183 cctggtggtgctgtagatctgacgacacagcgtatgaagacgcccacca 232
205101 cagggagaagcccccagacgacgacgagatccctgagggcccgcgccgg 205150
233 actactaccttccagccttgccgtctctgacctctgctctgctctct 282
205151 tgcctgtagcttggtggtgagcggaggtgtagatggtccacgtagcgtcc 205200
283 ggaatgccccctggagaggtctatgagatgtggtgcaactaccccttctgt 332
205201 acgctgaacggtgtgtagtctgagatgtagaggtggaagcacacgctcaaa 205250
333 cgggcccgtggtgctgacttcaagaacgcccctcttgagaccgtgtgct 382
205251 gagggtcgctcttgaaagttagcagcccaacgggtcccgaaacaagaaggtagt 205300
383 tcgacctcatctccagcatcaccacacgctcagcgtgagcgtacgtgccc 432
205301 tgcgcacatctccatagacctccacaggggtcattccaaagagcagagccagg 205350
433 atcctaacaccggttcgcgcacaaactcagagcagaccggcgccggccct 482
205351 agtcaagagaccgacaggtctgaagaggtagtagtgtggtggtcgtctcat 205400
```

```
483 cagatctctggcatgctgtggttctccgtgtctcttctccctggccca 532
205401 agcctgtgtctgcagaaatcaccaggcacaccaggaacattgccaatgacc 205450
533 acaccagcatctggcatcgaattccacttaccctcccaatggtccctg 582
205451 ccaccacaanaattggcacatcacacacagacaggggaggaagaagtgg 205500
583 gtcccaggttcggccaccctgtaacgtatcaagcccatgtgatctaca 632
205501 ctgcgcgaggtccgcagaggaagccagatactctcgtgctgttcag 205550
633 ttcatcatcaggtcaactctctctctatcttactctctcccatgactg 682
205551 gtgttctggaatgtagtcttctagtttctgctgtgtagatcagaagaat 205600
683 tcatcaggttctctactactcctcatatgacacagatgtagatctag... 729
205601 tctgaagtttctcatctccctgacatataatccaagaaggtcgtgacctccc 205650
```

GAP of reverse of: us-09-684-725-1, check: 1088 from: 1 to: 729

FROMIG of: /home/bobryen/big/US09684725.seq
sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1, check: 7472 from: 1 to: 32000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
Comphack: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000

Quality:	2494	Length:	32000
Ratio:	3.421	Gaps:	5
Percent Similarity:	38.546	Percent Identity:	38.546

Match display thresholds for the alignment(s):

1 = IDENTITY
- = 1

us-09-684-725-1 x version1 September 12, 2001 10:36

```
729 .....ctagatactcactcttgatgccatg 705
29351 gtaagtaatggaagctgtgttaaggaataatgaaggaagtgagg 29400
704 aggtcagtagaagacatgacatgacatgaggaagtagaataagaa 655
29401 ttgtaaagtagtgtagcgtgttaaggaagaaagagtttgagggaat 29450
654 g.gaggtgaccttgatgataatgtatgataccatgagcttgatgac 606
29451 gaggggaagatgtaagggcgagggatggtgttagatgagtcattggg 29500
605 gtacaggtgcccgaacctggaacagg.....gaccttgagggaagta 562
29501 ggaatagataataatagtgtaagaggttgatgaatgaatggaagag 29550
561 gtggaacttgatgccatggaatgctgtgttgscagggagaa..gagcac 514
29551 ggcagaagaagtttggaaggatcaatgtgatacgcggggctcattctaa 29600
513 ggaagaagcccagaagatgcccgaagatccttgaggcccgccgggtgc 464
29601 gaagttagagttacagataagtgatgataggaaagggaggaggaa 29650
463 tctgcagtttgcgcggaacgggtgttaggattgcccacgtacgctccacg 414
29651 ggaaggaagaaaggagggaggggaaggaaggaaggaaggaaggggg 29700
413 ctgacggtggtgacatgagatgagagcggaagcacaagctcaca.... 368
29701 agggaaagcagaagggaggaaggaatgacatcatcatcatgaagttg 29750
367 .....agaaggcgcgtcttgaagtagcagccacgggcccgaacaagaag 323
29751 tctctctggaatcttcacagacagctgtgataaagtgccaaactaagaact 29800
322 ggtgttgccgacatctcatagaccttcaggggagatcccaagagcag 273
29801 agaagcaggttctcttaataagcagcataaattgtcttaccatattat 29850
```

```
272 accagg...agtcagaagaccgccaagctgaaagagtagtagtgtg 227
29851 gccacggttaataataatlaagacagtttggacactcagattcttgg 29900
226 gcgtcttcatagcctgtgtcgcagaatcacccaggaagcacaagaacatg 177
29901 tgcaccaagaaggttagacacgtgcatgacaaaattctaattatata 29950
176 ccaatgaccccccacacaaaattggcacatacacccacagcaggggag 127
29951 ttatttagagatacaaatcttcaactctgtcacacaggggtggaatga 30000
126 gaagaagtgtcgtgcgcgaaggtccgcagagaaggaagccagatactc 77
30001 catgactcttgctcaatgacacactctgtctgtgttgtaacgagatttc 30050
76 tgcgttcaaggttctctggaatggatcttctagttctgtcgtgtagatc 27
30051 atgatacgctcttgagtagtgaaatlaacaggtgtgtgcccacacacc 30100
26 caggaagacatctgaagtttccat..... 1
30101 cagctaatttttctttttttttgattagtagagacaggtttgcatg 30150
```

GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729
FROMIG of: /home/bobryen/big/US09684725.seq
sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 32001 to: 64000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2575 Length: 32000
Ratio: 3.532 Gaps: 3
Percent Similarity: 38.409 Percent Identity: 34.842

Match display thresholds for the alignment(s):

IDENTITY
1

us-09-684-725-1 x version1 September 12, 2001 10:44

```
729 .....ctagatactcactctcgtgctgcatgaggtgtagtaggacactgat 685
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48451 atgggtgggaatttcaggagatgtgtcaggttccttgaaacacgtgaa 48500
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
684 gacagtcctgggagaggtgagatgagaaagaggtgacgtgagatgagaa 635
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48501 cctccagatgaaatcagagagctgacgagcaatgtatataatgtttaatcg 48550
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
634 aattgtagatccacatggtctgtgtagacgttacaggtggtccgaacctggg 585
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48551 gggacaaccacaatggtcaggtgtaggtctgtagtcttgaggaggttccct 48600
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
584 accagggaccatttggggaggtgagtggaacttgatgacatgagtcgtgc 535
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48601 ccaatggaaaagaaagcaggttttgagatttctgttgaggttacattt 48650
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
534 gttggcagggagagagacgagagagccccaagacgaltgccgagatcc 485
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48651 ccaataagaaagaaaggtcgtcatctgcatgtgactgtcatatttctgatat 48700
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
484 tgaagggtccggtccggtgctgtcgtcagttt.....ggcgc 449
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48701 gacagttcctccactagatgtcgtgaggttaaggtgtagcagggagagcg 48750
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
448 ggaacgggtgtgagatggtgcacgtgacgttcacacgtgacggtgtgtatg 399
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48751 agaaataggttgagagcagcagactagcaattaggtgaaggccaccgg 48800
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
398 ctgaagatgtgaggtgagacacacaggtctcaaaagaggtccgtcttgaagla 349
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48801 gttgattcgtgtgagagagcaagactcttgaaagtgcacactcttgact 48850
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
348 gcaagcccaaggtccgaacaaagaaaggtgagtgcacaa.....tct 305
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48851 acttctcacaagccttgcctcttagagttacttcaactgtccagttgcttaa 48900
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
304 catagacctcaggtggtcattccaagagcagagcagagaggtcagagacc 255
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48901 catctgacctcagctcagtgatgtaagtgtacgtacataataatgtgtct 48950
```

```
254 gccaggtcgaagagtagtagtgtgtg.....ggcgtcttcatagccttg 210
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48951 tacactgaaagtagtaataccactagatgaactctacgagagatatatactct 49000
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
209 tgcgtcagaatcacaacagacacagacaltgccaaltgaccccaacac 160
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49001 tctgttaacatttaggtctccttcacatcaggtgagtagagctgtattaa 49050
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
159 aaaaattgacatatcacacacagacagcgggaggaagaagtgtgtgcgc 110
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49051 ggtccaccagccttacatcagttccccaagtgaacactccccccttggggn 49100
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
109 gagggtccgagaggaagccagatactctcgtgtgtgtgtgtgtgttc 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49101 gggggggnngggggggggggggggnngnngnngtgcgtgtgtgtgtc 49150
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
59 tgaatgattcttctagtttctgtgtgtagatccagaagaatcttgag 10
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49151 gatnnagaatgtnnntcngntgagngnngnngnngnngnngatcatgt 49200
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
9 ttlttccat..... 1
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49201 ctctgacctgaatgtgttttcttcttcagcatatctgcctccttgtat 49250
```

GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729

FROM: /home/bobryen/big/US09684725.seq
Sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 64001 to: 96000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
Compcheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	2425	Length:	32002
Ratio:	3.326	Gaps:	2
Percent Similarity:	34.938	Percent Identity:	34.938

Match display thresholds for the alignment(s):

:- IDENTITY
:- 5
:- 1

us-09-684-725-1 x version1 September 12, 2001 10:38

```

729 .....ctagatactactcttgatgcataggtagtagagagacacgtat 685
      | | | | | | | | | | | | | | | | | | | | | | | | |
68401 tgactccataatccatgaatgctccctccctgagcgaataatitgaa 68450
      | | | | | | | | | | | | | | | | | | | | | | | | |
684 gatcatatggaggaggtagaatagaagaggtgacccgtgatatga 635
      | | | | | | | | | | | | | | | | | | | | | | | | |
68451 gtgtgctctgaacaacacctgtgtgcaagcactgtccctaactatac 68500
      | | | | | | | | | | | | | | | | | | | | | | | | |
634 aattgataicacatggtcttgatgacccgtacaggtgcccgaacctggg 585
      | | | | | | | | | | | | | | | | | | | | | | | | |
68501 agatctgtgtctgtgatataccagacccctccatgaagctgataag 68550
      | | | | | | | | | | | | | | | | | | | | | | | | |
584 accagggaccattgggggaagtatgtaactgtgcatatgactgtgt 535
      | | | | | | | | | | | | | | | | | | | | | | | | |
68551 gtccagccccaagatgataccagagacagcatagaanaatgattgtgg 68600
      | | | | | | | | | | | | | | | | | | | | | | | | |
534 gtggcagggagagagacagcagagcccagacagatgcccagagatcc 485
      | | | | | | | | | | | | | | | | | | | | | | | | |
68601 ggaacatttaactcagcctctctctgtgtgatgagatcttaagaagctc 68650
      | | | | | | | | | | | | | | | | | | | | | | | | |
484 tgagggcccgccgctgtgtcgtcagtttgcgcggaacggtgtatgg 435
      | | | | | | | | | | | | | | | | | | | | | | | | |
68651 tacatgaggttaactcatcttacttaactataaccctataataacca 68700
      | | | | | | | | | | | | | | | | | | | | | | | | |
434 atggccacgtatgcgtccacgctgaaggtgtgtatgtctgaagatggggc 385
      | | | | | | | | | | | | | | | | | | | | | | | | |
68701 ctcatagatggaaaacatgaagcctaagaagaatgtaaaaacagacaa 68750
      | | | | | | | | | | | | | | | | | | | | | | | | |
384 gaaagcacacggctccaaagaagggcgtcttgaagtagacagccagggcc 335
      | | | | | | | | | | | | | | | | | | | | | | | | |
68751 aggcagtaactatataataatggaacttggccacaagctcagcaaac 68800
      | | | | | | | | | | | | | | | | | | | | | | | | |
334 cgaacaagaagaagggtagttgcgcacatctatagacctcaggggacat 285
      | | | | | | | | | | | | | | | | | | | | | | | | |
68801 tgcacagaanaacaaacttgcctatctacatgtgacccagccagaaaca 68850
      | | | | | | | | | | | | | | | | | | | | | | | | |
284 ccaagggagcagacagaggttcagagacccgacggctgaagaaggtatga 235
      | | | | | | | | | | | | | | | | | | | | | | | | |
68851 gcctctgttaagtcagcgtctgaaggaagctgaactgtcatctttagtaa 68900

```

```

234 gtgtgtggcgctctcatagcctgtgtgtgcagaataccagcgaca... 188
      | | | | | | | | | | | | | | | | | | | | | | | | |
68901 aatctaggaagaagcctaacaataatcttctgttaacaatacagccccaatag 68950
      | | | | | | | | | | | | | | | | | | | | | | | | |
187 ccaggacattgccaatgacccccaacaaatggcacatacacaca 138
      | | | | | | | | | | | | | | | | | | | | | | | | |
68951 ccagacttgacgaatga..cctagagttgaaattgagttcaltgatatgtt 68998
      | | | | | | | | | | | | | | | | | | | | | | | | |
137 gacacgggggaagaagaagtgtgtgcgcagaggtccgcagagaagaagccag 88
      | | | | | | | | | | | | | | | | | | | | | | | | |
68999 gtccctatttccaaacttaggacccagcagagaagaatgaataagcttcc 69048
      | | | | | | | | | | | | | | | | | | | | | | | | |
87 atactcctcgtgtgtgtcaggtgttctctggaatggaatctctagttct 38
      | | | | | | | | | | | | | | | | | | | | | | | | |
69049 caccatctcagagagctgcctgatttctaggtagcaaccctccagcttct 69098
      | | | | | | | | | | | | | | | | | | | | | | | | |
37 gctgtagatccaggaagcattctgaagtcttccat..... 1
      | | | | | | | | | | | | | | | | | | | | | | | | |
69099 ccagtagtctcacaacagccttcttcttcttctcactataagcttatac 69148

```

GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729

FROM: of: /home/bobryen/Dig/US09684725.seq
sequence 1, application us/09684725

general information:

applicant: lee harland

title of invention: novel polypeptide

file reference: pcs10361adam

to: version1 check: 7472 from: 96001 to: 128000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2532 Length: 32009

Ratio: 3.473 Gaps: 6

Percent Similarity: 40.417 Percent Identity: 40.417

Match display thresholds for the alignment(s):

IDENTITY
1

us-09-684-725-1 x version1 September 12, 2001 10:53

```

729 .....ctagatactactctgagtgcca 707
127201 atagctgcatgcatcattagatgatttgaacaagattaagtcgtttaa 127250
706 tgaagctagtaagaagacactgatacagtcacatgaggaaggtagaatagg 657
127251 gcatcaaatcaaccagagaggtctctcctcgtggaacaagtcagaagcgg 127300
656 aaggaagtgacctgatactgaatctgtagtc..cacatggcttgatg 609
127301 gggcagcagaagctggaataaaaaaacggcttaagaagcatttg 127350
608 accgtacaggtggccgaacctgggaccaaagga.....cccatggggaa 565
27351 atagcccaagtgaggagaagagtagcttgattagatgtagtcagaa 127400
564 gtaatggaacttgatgcatgctgtgtctgtggaaggaagaagca 515
127401 atgtttgagaagtgctcagaaggtgagatgtattcaggagatcaagaa 127450
514 cggagaagccccaagcagatgccgaagatccctgaaggcccgccgggtg 465
127451 agaaagtgttcaataga..gaggagaattttaaaaaatcaatgc...tg 127495
464 ctctgcgaatttcggcgcgaaacgggtgtagatggccacgttagcgtc... 418
127496 ctgagaagcttgaacaagaagaagataaaltgatacttgaaggtcatt 127545
417 .....cagcctgaacgtgctgcatgctgaggaatggaagcgaagcacagc 374
127546 ggtgagccttgatgagagtggtcttccctggaacaatggaagaaagcctg 127595
373 tctcaagaaggcgccgtcttgtaagtagcagccacggcgccgaacaagaa 324
127596 agtgaagtgatcccaagaagaagtgaaatagagatgtggagcaaaaaa 127645
323 gggtagtctggcccaatctcatagacccacggggcatccaaggagcag 274
127646 tatagattgagcaatttctgacttaaaagaagcatatcatgagag 127695

```

```

273 gaccagaagtcagaagaccgccaagctgaagaagtagtagtggggcg 224
127696 gattataacgattataacgtgaatgataataacttaagaagtataca 127745
223 tctcatagctgtgtgtcgcagaatcacaccaggcacaccagaacattgcc 174
127746 tattattttaaacacacacaaagaatagaagaatgtgacctatatt 127795
173 atgaccccaaccacaanaaaitggcacatcacccacagacagggaggaa 124
127796 tctctctctccatccatt....aactactccctatgctcagggaagaag 127841
123 gaagtgtctgcgcgaaggtccgcagaagaagagccagatactcctcgtgc 74
127842 aaagaccttcgtatgatatgggacaaaatgaccttgggaagacacagc 127891
73 tgttaagtggttctggaatgatacttctgattctgtctgtatgacag 24
127892 aggcacttgccttaagaagctctagatggagcagcggggtaaaa 127941
23 gaagattctgaagtcttcacat..... 1
127942 acagcagaacaacactgagcaagcctctctagtcggttatagatctc 127991

```


GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729
FROMIG of: /home/bobryen/b1g/US09684725.seq
sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 128001 to: 160000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
Compcheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	2443	Length:	32006
Ratio:	3.351	Gaps:	6
Percent Similarity:	38.728	Percent Identity:	38.728

Match display thresholds for the alignment(s):

IDENTITY
1

us-09-684-725-1 x version1 September 12, 2001 10:45

```
729 .....ctagatactcaactctgaagtcga 707
156251 aggtatttgagagatgacgtgagatcatcattataaagatttggcaca 156300
706 tgaagtagtagagacactgtacgtacgtacgtgagaggtagaatag 657
156301 gtgcacaagaagtaactcaatattgttggtcttaaatatagcata 156350
656 aaggaggtgacctgtgattgaattgtlagaatccacatggct. tgaatga 608
156351 attgttaataagaagcaagaacataatacaagaatgagctctgttg 156400
607 ccgtacacgggtgcccgaaccttggaacagggaacccattggggaaatggtg 558
556401 acaaaaatctctggaacctgagtcagatcatattctgagagagtgta 156450
557 aactgtatgcattgactgtgtgttggtgagaggaagacagagaa 508
156451 tatcttcaagaatgaataataatagagagatggaagg...gaaggtc 156496
507 gccccagaagatgcccgaagatccctgagggcccggcgctgcttgca 458
156497 attccaagaagcaggtgtgacagcatggcggtcaaaggagccggcagca 156546
457 gtttgggcgggaacgggtgtgagatggtgacatgctgctcaccgtgacg 408
156547 gtgctctggaagtgacagagag..cgataagcagtgtagcttgaagtcagag 156594
407 gtgtgtatgtcgaagatggaagcgaagcacaacgggtctcaagaagagccgt 358
156595 gtaaggatagtgagagcagatgaggggtgtggtcttgatcccaagcgcca 156644
357 ctltgaag.....tagcagcccaacgggcccgaacaagaagaaggtatgtgc 314
156645 caactaagattgtctgatatctgagggcccccacacaaaaaaataatt 156694
313 gccacatctctatagacctccacagggcatctcaagaagagaccagagag 264
156695 ttgaaaaaaggggggccccaataaaggitttaagagggggagcaacatgc 156744
```

```
263 tcagagaaccgcaagctgaagaagtagtagttgtgtggcgtcttcatagc 214
156745 tctgtctgcattttaagaagaatccctctgtgcagtttgacgcaggggtgaa 156794
213 ctgtgtctgcagaatcaccaaggcacaccagacattggccaatg...acc 168
156795 tttaagaacaagaattcaggaagcagggagacaattaggaagctgtgg 156844
167 cccacacaaaaaattgacacatcacacacacacggggaggaagaagt 118
156845 aatagttcagatgagaggtgtgacaaactgaactaaggcaatgtgtgca 156894
117 gctggccgaagtcgcgacaggaagggccagatactcctcggtgctgtca 68
156895 gagacaaagaaggaaataactataatgaataatlttaagggtgattctca 156944
67 ggtgttctctgaatgtat..ctctagttctgtgtgtagatccaagaag 20
156945 aagatgtgagacatgattgattagacgttgaggaagaggttgcttgag 156994
19 catctgaagtttccat..... 1
156995 gttctgacacagtcgtcctaagtacgttggtggcccttactttaaagg 157044
```

GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729

FROM: /home/bobyen/Big/US09684725.seq
Sequence 1, application us/09684725

General information:

Applicant: lee harland

Title of invention: novel polypeptide

File reference: pcs10361adam

to: version1 check: 7472 from: 160001 to: 192000

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 2516 Length: 32002
Ratio: 3.451 Gaps: 7
Percent Similarity: 41.816 Percent Identity: 41.816

Match display thresholds for the alignment(s):

:- IDENTITY
:- 5
:- 1

us-09-684-725-1 x version1 September 12, 2001 10:48

```
729 .....ctagatactcaactctgagtcgcaatgaggtagtagagga 692
184301 ctccacaagcgtcgcattccatccagagcatgacaatctgtt 184350
691 cactgagtcacagtcgtgggaggaagtagaataaggaaggtgacctg 642
184351 ctgggataaggaatctgtgtagtgaaactccctgactgcagtcac 184400
641 atgagt.....aaattgataccacatggcgctgatatgacgtacag 600
184401 cataggtctctgcaggaagacacatcagcgtgtgtgctcattct 184450
599 gtgagcgaacctg.....gaacaggaccattggggaag 564
184451 gcggtccaaacctgcatgtcttacaacatcctgcatgcaatttgtat 184500
563 tagtggaaactgagtcagatgctgtgtgtggcagggagaagagcac 514
184501 ttaaaataatcagagacatctcaatcttattcgtagcaaatagttcag 184550
513 ggagaagccccagacgaltccaggatccttgaggccccggcggtgc 464
184551 ggggtctccataacatacaaaagcttcaagttgtttacagcatlta 184600
463 tctgagtttggcgagaaaggtgtagatggcagtagcgctccag 414
184601 aaaaaaaatlaagcctaacttctgtctcagctgtatgtgacacaa 184650
413 ctgacggtggtgagtcgtagatgagcgaagcacagcgtctcaagag 364
184651 gattcaaaatcaatctctcaa..gattccaacacagttccagctatcc 184698
363 ggcgctcttgaaagtagcagccacgagccgaacaaagaaggtagttgc 314
184699 agaccatctgcataaataagcacaatagtcacaccaaagaacttactct 184748
313 gcaaatctatagaactccacaggggcatctcaagagcaggaacagagag 264
184749 ctgacataagaggtctcggtgacctaataatgacatgcaatgacag 184798
```

```
263 tcaagagaccgc.....agctgaagaggtagtagttgtg 228
184799 atataaagacctcagactggaagagagaagtgaagccctgttctg 184848
227 ggcgtctcatagcctgtgtgtgcagaatacacaagccacacacagacat 178
184849 tagttgtgtcagaatctgtgtgtgcagatgagcagatggccgaataagt 184898
177 gccaatgaccccccacacaaaattgacacatacacacaagaacagcgga 128
184899 cacaagttccaaacctgacctgtgtcatattcactagtgatctgtt 184948
127 ggaagaagtgtgtgcgcga.....gttcgcagaggaagccaga.... 87
184949 aaaaagaattccctcagcagacttaactagatctcagcggtgcccgaat 184998
86 ..tactctcgtgtgtgt.....caggtgttctggaaatgatatc 48
184999 aagtacctcaggggtgatttttatgtcatccgtggaatttggagtcattgt 185048
47 tctagttctgtgtgtagatccaggaagcattctgaagttttccat... 1
185049 tctaagttataagcctctcagaaccacataatgtgtgtcctccattgt 185098
```

GAP of reverse of: us-09-684-725-1 check: 1088 from: 1 to: 729
FROMIG of: /home/bobyren/big/US09684725.seq
sequence 1, application us/09684725

general information:
applicant: lee harland
title of invention: novel polypeptide
file reference: pcs10361adam

to: version1 check: 7472 from: 192001 to: 218807

Symbol comparison table: /opt/gcg/gcgcore/data/rundata/nwsgapdna.comp
Compcheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	7290	Length:	26807
Ratio:	10.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

1 = IDENTITY
- = 1

us-09-684-725-1 x version1 September 12, 2001 10:41

```
729 .....ctagatactact 717
204851 tgaataaaggagatgctgctcagccaccagccttagatactact 204900
716 ctgagtcgcaatgagtagtagagacacttgatgacatggtgggaagag 667
204901 ctgagtcgcaatgagtagtagagacacttgatgacatggtgggaagag 204950
666 gtagaataaggaaaggatgacctgtagatgaaattgtagatccacatgg 617
204951 gtagaataaggaaaggatgacctgtagatgaaattgtagatccacatgg 205000
616 gcttgatgaacctgtagatggtggccgaacctgtagacagagaccattgggg 567
15001 gcttgatgaacctgtagatggtggccgaacctgtagacagagaccattgggg 205050
566 aagtagtggaaacttgatgcatgtagatggtggtggcgaaggagaagag 517
205051 aagtagtggaaacttgatgcatgtagatggtggtggcgaaggagaagag 205100
516 caaggaagaagcccgagacgagatgctgagggcccgccggg 467
205101 caaggaagaagcccgagacgagatgctgagggcccgccggg 205150
466 tgcctcgaagtttggcgggaacgggtgtagatggtccacgtagcgtcc 417
205151 tgcctcgaagtttggcgggaacgggtgtagatggtccacgtagcgtcc 205200
416 acgctgacggtgtagatgtagatgtagagcgaagcgaacggtctcaaa 367
205201 acgctgacggtgtagatgtagatgtagagcgaagcgaacggtctcaaa 205250
366 gagggcggtctgtagatgtagcgaacgggcccgaacaagaaggtagt 317
205251 gagggcggtctgtagatgtagcgaacgggcccgaacaagaaggtagt 205300
316 tgccgcacatctcagacctcaggggcatctcaagaagagagaccagg 267
205301 tgccgcacatctcagacctcaggggcatctcaagaagagagaccagg 205350
```

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266 aggtcagaagaccgccaaggctgaagagtagtagttggtggcgcttcat 217
205351 aggtcagaagaccgccaaggctgaagagtagtagttggtggcgcttcat 205400
216 agcctgtgtctgcaagaatcaccagggcacacaggaacattgccaatgacc 167
205401 agcctgtgtctgcaagaatcaccagggcacacaggaacattgccaatgacc 205450
166 ccaccacaaaattggcacaatacacaagacagcgagggaagaagatgg 117
205451 ccaccacaaaattggcacaatacacaagacagcgagggaagaagatgg 205500
116 ctgcgcgaaggtccgcaaggaaggccagatctcctggtgctgttag 67
205501 ctgcgcgaaggtccgcaaggaaggccagatctcctggtgctgttag 205550
66 gttttctggaatgatalcttctagtttctgtgtgtagatccagaagaat 17
205551 gttttctggaatgatalcttctagtttctgtgtgtagatccagaagaat 205600
16 tctgaagtttccat..... 1
205601 tctgaagtttccatccctgacatlaaatccaagcgctgagcctccc 205650
```